



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

RID: 1064951850-6704-3160357.BLASTQ3

Query=

(659 letters)

Blast w/ Hep III
No hit for Hep II

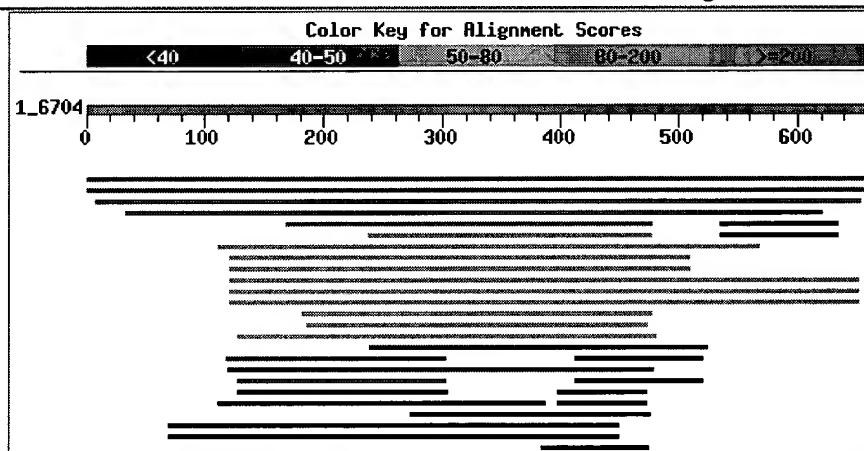
Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF

1,544,151 sequences; 499,133,508 total letters

[Taxonomy reports](#)

Distribution of 31 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:					Score (bits)	E Value
gi	924925	gb	AAB18278.1	heparinase III protein	1295	0.0
gi	2120581	pir	JC4910	heparin-sulfate lyase (EC 4.2.2.8) -...	1275	0.0
gi	29350065	ref	NP_813568.1	heparinase III protein [Bacter...	536	e-151
gi	29350070	ref	NP_813573.1	heparinase III protein, hepari...	290	5e-77
gi	23053377	ref	ZP_00079586.1	COG5360: Uncharacterized pro...	80	8e-14
gi	23117139	ref	ZP_00101341.1	COG5360: Uncharacterized pro...	68	6e-10
gi	30265295	ref	NP_847672.1	conserved domain protein [Baci...	65	5e-09
gi	25011924	ref	NP_736319.1	Unknown [Streptococcus agalact...	65	6e-09
gi	22538035	ref	NP_688886.1	conserved hypothetical protein...	64	6e-09
gi	15674701	ref	NP_268875.1	hypothetical protein [Streptoc...	63	2e-08
gi	21909978	ref	NP_664246.1	conserved hypothetical protein...	62	5e-08
gi	19745729	ref	NP_606865.1	hypothetical protein [Streptoc...	59	2e-07
gi	23016043	ref	ZP_00055804.1	COG5360: Uncharacterized pro...	58	5e-07
gi	20559784	gb	AAM27563.1	AF498401_11 ORF_11; similar to Pr...	55	6e-06
gi	22657440	gb	AAN04237.1	hypothetical protein Ste12 [Stre...	50	1e-04
gi	27381410	ref	NP_772939.1	blr6299 [Bradyrhizobium japoni...	50	2e-04
gi	29376772	ref	NP_815926.1	conserved hypothetical protein...	48	5e-04
gi	20560019	gb	AAM27770.1	AF498414_12 ORF_12 [Pseudomonas a...	47	0.001

gi	21218931	ref	NP_624710.1	hypothetical protein SCF62.14 ...	45	0.005
gi	17549231	ref	NP_522571.1	CONSERVED HYPOTHETICAL PROTEIN...	38	0.61
gi	21397739	ref	NP_653724.1	hypothetical protein predicted...	37	0.88
gi	21221922	ref	NP_627701.1	hypothetical protein [Streptom...	37	1.2
gi	15900259	ref	NP_344863.1	hypothetical protein, interrup...	37	1.6
gi	15902341	ref	NP_357891.1	Hypothetical protein [Streptoc...	36	2.4
gi	22124624	ref	NP_668047.1	hypothetical [Yersinia pestis ...	36	2.9
gi	16123620	ref	NP_406933.1	hypothetical protein [Yersinia...	36	2.9
gi	32141206	ref	NP_733607.1	hypothetical protein [Streptom...	35	5.7
gi	13474921	ref	NP_106491.1	nitrogenase molybdenum-iron pr...	35	5.9
gi	7479860	pir	T36083	hypothetical protein SCE134.01c - St...	35	6.1
gi	16519994	ref	NP_444114.1	NifK1 [Rhizobium sp. NGR234] >...	34	6.7
gi	29345536	ref	NP_809039.1	hypothetical protein [Bacteroi...	34	7.1

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|924925|gb|AAB18278.1| heparinase III protein
Length = 659

Score = 1295 bits (3352), Expect = 0.0

Identities = 647/659 (98%), Positives = 647/659 (98%)

```

Query: 1  MTTKIFKRIIVFAVIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKAVAAGNXXXXX 60
          MTTKIFKRIIVFAVIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKAVAAGN
Sbjct: 1  MTTKIFKRIIVFAVIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKAVAAGNYDDAA 60

Query: 61  XXXXXXXREKSKAREPDFSNAEKPADIRQPIDKVTREMADKALVHQFQPHKGYGFDYGK 120
          REKSKAREPDFSNAEKPADIRQPIDKVTREMADKALVHQFQPHKGYGFDYGK
Sbjct: 61  KALLAYYREKSKAREPDFSNAEKPADIRQPIDKVTREMADKALVHQFQPHKGYGFDYGK 120

Query: 121  DINWQMWPVKDNEVRWQLHRVKWWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQ 180
          DINWQMWPVKDNEVRWQLHRVKWWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQ
Sbjct: 121  DINWQMWPVKDNEVRWQLHRVKWWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQ 180

Query: 181  DNDKFVWRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQQADYLSYHAEQGN 240
          DNDKFVWRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQQADYLSYHAEQGN
Sbjct: 181  DNDKFVWRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQQADYLSYHAEQGN 240

Query: 241  HRLFEAQRNLFAGVSFPEFKDSPRWRQTGISVLNTEIKKQVYADGMQFELSPIYHVAAID 300
          HRLFEAQRNLFAGVSFPEFKDSPRWRQTGISVLNTEIKKQVYADGMQFELSPIYHVAAID
Sbjct: 241  HRLFEAQRNLFAGVSFPEFKDSPRWRQTGISVLNTEIKKQVYADGMQFELSPIYHVAAID 300

Query: 301  IFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALISISLDPYNTPMFGDSWITDKNFRMAQ 360
          IFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALISISLDPYNTPMFGDSWITDKNFRMAQ
Sbjct: 301  IFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALISISLDPYNTPMFGDSWITDKNFRMAQ 360

Query: 361  FASWARVFANQAIKYFATDGKQGKAPNFLSKALSNAGFYTFRSGWDKNATVMVLKASPP 420
          FASWARVFANQAIKYFATDGKQGKAPNFLSKALSNAGFYTFRSGWDKNATVMVLKASPP
Sbjct: 361  FASWARVFANQAIKYFATDGKQGKAPNFLSKALSNAGFYTFRSGWDKNATVMVLKASPP 420

Query: 421  GEFHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNWRQTRIHSTLTLDNQNMV 480
          GEFHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNWRQTRIHSTLTLDNQNMV
Sbjct: 421  GEFHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNWRQTRIHSTLTLDNQNMV 480

Query: 481  ITKARQNKWETGNNLDVLTYNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATGNLGVHW 540
          ITKARQNKWETGNNLDVLTYNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATGNLGVHW
Sbjct: 481  ITKARQNKWETGNNLDVLTYNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATGNLGVHW 540

Query: 541  QLKEDSNPVFDKTKNRVYTTYRDGNNLMIQSLNADRTSLNEEEGKVSYYVNKELKRPAFV 600
          QLKEDSNPVFDKTKNRVYTTYRDGNNLMIQSLNADRTSLNEEEGKVSYYVNKELKRPAFV
Sbjct: 541  QLKEDSNPVFDKTKNRVYTTYRDGNNLMIQSLNADRTSLNEEEGKVSYYVNKELKRPAFV 600

```

Query: 601 FEKPKKNAGTQNFVSIVYPYDGQKAPEISIRENKGNDFEKGKLNLTTLTINGKQQLVLP 659
 FEKPKKNAGTQNFVSIVYPYDGQKAPEISIRENKGNDFEKGKLNLTTLTINGKQQLVLP
 Sbjct: 601 FEKPKKNAGTQNFVSIVYPYDGQKAPEISIRENKGNDFEKGKLNLTTLTINGKQQLVLP 659

☐ >gi|2120581|pir||JC4910 heparin-sulfate lyase (EC 4.2.2.8) - Flavobacterium hepa
 Length = 659

Score = 1275 bits (3299), Expect = 0.0
 Identities = 639/659 (96%), Positives = 639/659 (96%)

Query: 1 MTTKIFKRIIVFAVIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKAVAAGNXXXXX 60
 MTTKIFKRIIVFAVIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKAVAAGN
 Sbjct: 1 MTTKIFKRIIVFAVIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKAVAAGNYDDAA 60

Query: 61 XXXXXXREKSKAREPDFSNAEKPADIRQPIDKVTREMADKALVHQFQPHKGYGYFDYGK 120
 REKSKAREPDFSNAEKPADIRQPIDKVTREMADKALVHQFQPHKGYGYFDYGK
 Sbjct: 61 KALLAYYREKSKAREPDFSNAEKPADIRQPIDKVTREMADKALVHQFQPHKGYGYFDYGK 120

Query: 121 DINWQMWPVKDNEVRWQLHRVKWWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQ 180
 DINWQMWPVKDNEVRWQLHRVKWWQ ATGDEKYAREWVYQYSDWARKNPLGLSQ
 Sbjct: 121 DINWQMWPVKDNEVRWQLHRVKWWQLWPWFITATGDEKYAREWVYQYSDWARKNPLGLSQ 180

Query: 181 DNDKFVWRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQQADYLSHYAEQGN 240
 DNDKFVWRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQQADYLSHYAEQGN
 Sbjct: 181 DNDKFVWRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQQADYLSHYAEQGN 240

Query: 241 HRLFEAQRNLFAGVSFPEFKDSPRWRTGISVLNTEIKKQVYADGMQFELSPIYHVAAID 300
 HRLFEAQRNLFAGVSFPEFKDSPRWRTGISVLNTEIKKQVYADGMQFELSPIYHVAAID
 Sbjct: 241 HRLFEAQRNLFAGVSFPEFKDSPRWRTGISVLNTEIKKQVYADGMQFELSPIYHVAAID 300

Query: 301 IFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALISISLPDYNTPMFGDSWITDKNFRMAQ 360
 IFLKAYGSAKRV LEKEFPQSYVQTVENMIMALISISLPDYNTPMFGDSWITDKNFRMAQ
 Sbjct: 301 IFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALISISLPDYNTPMFGDSWITDKNFRMAQ 360

Query: 361 FASWARVFPANQAIKYFATDGKQGKAPNFLSKALSNAAGFYTFRSGWDKNATVMVLKASPP 420
 FASWARVFPANQAIKYFATDGKQGKAPNFLSKALSNAAGFYTFRSGWDKNATVMVLKASPP
 Sbjct: 361 FASWARVFPANQAIKYFATDGKQGKAPNFLSKALSNAAGFYTFRSGWDKNATVMVLKASPP 420

Query: 421 GEFHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNWRQTRIHSTLTLDNQNMV 480
 GEFHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNWRQTRIHSTLTLDNQNMV
 Sbjct: 421 GEFHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNWRQTRIHSTLTLDNQNMV 480

Query: 481 ITKARQNKWETGNNLDVLTYNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATGNLGVHW 540
 ITKARQNKWETGNNLDVLTYNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATGNLGVHW
 Sbjct: 481 ITKARQNKWETGNNLDVLTYNPSYPNLDHQRSVLFINKKYFLVIDRAIGEATGNLGVHW 540

Query: 541 QLKEDSNPVFDKTKNRVYTTYRDGNNLMIQSLNADRTSLNEEEGKVSIVYNKELKRPAFV 600
 QLKEDSNPVFDKTKNRVYTTYRDGNNLMIQSLNADRTSLNEEEGKVSIVYNKELKRPAFV
 Sbjct: 541 QLKEDSNPVFDKTKNRVYTTYRDGNNLMIQSLNADRTSLNEEEGKVSIVYNKELKRPAFV 600

Query: 601 FEKPKKNAGTQNFVSIVYPYDGQKAPEISIRENKGNDFEKGKLNLTTLTINGKQQLVLP 659
 FEKPKKNAGTQNFVSIVYPYDGQKAPEISIRENKGNDFEKGKLNLTTLTINGKQQLVLP
 Sbjct: 601 FEKPKKNAGTQNFVSIVYPYDGQKAPEISIRENKGNDFEKGKLNLTTLTINGKQQLVLP 659

☐ >gi|29350065|ref|NP_813568.1| heparinase III protein [Bacteroides thetaiotaomicr
 gi|29341977|gb|AA079762.1| heparinase III protein [Bacteroides thetaiotaomicron V
 Length = 666

Score = 536 bits (1380), Expect = e-151
 Identities = 283/667 (42%), Positives = 397/667 (59%), Gaps = 32/667 (4%)

Query: 8 RIIVFAVIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKAVAAGNXXXXXXXXXXXXX 67
 + IV A G AQ + + F +NL+Y GLEKV G
 Sbjct: 6 KYIVLLTTFACFVGKGYAQ--ELKSEVFSLLNLDYPGLEKVKALHQEGKDEDAAKALLDYY 63

Query: 68 REKSKAREPDFSNAEKPADIRQPIDKVTREMADKALVHQFQPHKGYG-YFDYGKDINWQM 126
R ++ + PD N +K I K ++ AD L H F HKGY ++YG+DINWQ
Sbjct: 64 RARTNVKTPDI-NLKKIT-----IGKEEQWADDGLKHTFFVHKGYQPSYNYGEDINWQY 117

Query: 127 WPKVDNEVRWQLHRVKWWQAMALVYHATGDEKYAREWVYQYSDWARKNPL-----GL 178
WPKVDNE+RWQLHR KW+ M Y +GDEKYA+EW YQY DW +KNPL L
Sbjct: 118 WPKVDNELRWQLHRHKWFTPMGKAYRVSGDEKYAKEWAYQYIDWIKKNPLVKMDKKEYEL 177

Query: 179 SQD-----NDKFVWRPLEVSDRVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQQADY 230
D N +F WRPLEVS+R+Q F LF+ SP+FTP FL EFL +YH+ A +
Sbjct: 178 VSDGKIKGEVENVRFAWRPLEVSNRLQDQTTQFQLFLPSPSFTPDFLTEFLVNYHKHAVH 237

Query: 231 LSTHYAEQGNHRLFEAQRNLFAGVSFPEFKDSPRWQRGTGISVLNTEIKKQVYADGMQFEL 290
+ +Y++QGNH LFEAQR ++AG FPEFK++P WR++GI +LN E+ QVY DG QFEL
Sbjct: 238 ILANYSDQGNHLLFEAQRMIYAGAFFPEFKEAPAWRKSGIDILNREVNQVYNDGGQFEL 297

Query: 291 SPIYHVAADIFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALISISLPDYNTPMFGDSW 350
P YH+AAI+IF KA G A EFPQ Y+ T+E MIM +IS PDY P F D+
Sbjct: 298 DPHYHLAAINIFCKALGIADVNGFRNEFPQYEYLDITIEKMIMFYANISFPDYTNPCFSDAK 357

Query: 351 ITDKNFRMAQFASWARVFPANQAIKYFATDGKQKAPNFLSKALSNAAGFYTFRSGWDKNA 410
IT+K + + +W+++FP N+ IKY ATDGK+G P+++SK +GF+ FR+ W +A
Sbjct: 358 ITEKKEMLKNYRAWSKLFPKNETIKYLATDGKEGALPDYMSKGLKSGFFVFRNSWGMDA 417

Query: 411 TVMVLKASPPGEFHAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIMKLRNWYRQTRIHS 470
T MV+KA P G +H QPDNGTFE++ G+N PD+G +VY+G+ +M+ RNW+RQT +H+
Sbjct: 418 TQMVVKAGPKGFWHCQPDNGTFEMWFNGKNLFPDGSYVYAGEGEVMEQRNWHRQTSVHN 477

Query: 471 TLTLDNQNMVITKARQNKWETGNNLDVLTYNPSYPNLDHQRSVLFINKKYFLVIDRAIG 530
T+TLDN+N+ T++ W+ N+ L NPSY N H+RSV F++ YF+++D G
Sbjct: 478 TVTLDNKNLETTESVTKLWQPEGNIQTLVTENPSYKNFKHRRSVFFVDNTYFVIVDEVSG 537

Query: 531 EATGNLGVHWQLK--EDSNPVFDKTKNRVYTTYRDGNNLMIQSLNADRTSLNEEEGKVS 588
A G++ +H+Q+ E +N D T T + DG+N+ +Q + S+ +E G S
Sbjct: 538 SAKGSVNLHYQMPKGEIANSREDMT---FLTQFEDGSNMKLQCFGPEGMSMKKEPGWCST 594

Query: 589 VYNKELKRPAFVFEKPKKNAGTQNFVSIVYPY-DGQKAPEISIRENKGNDFEKGKLNLT 647
Y K KR F K N +++++YP AP+ + K F++ L + +
Sbjct: 595 AYRKRYKRMNVSFNVKKNENAVRYITVIYPVKKSADAPKFDK-FKNKTFDENGLEIEV 653

Query: 648 TINGKQQ 654
+NGK+Q
Sbjct: 654 KVNGKKQ 660

☐ >gi|29350070|ref|NP_813573.1| heparinase III protein, heparitin sulfate lyase [E
thetaitaomicron VPI-5482]
gi|29341982|gb|AAO79767.1| heparinase III protein, heparitin sulfate lyase [Bacte
thetaitaomicron VPI-5482]
Length = 702

Score = 290 bits (743), Expect = 5e-77
Identities = 191/624 (30%), Positives = 306/624 (49%), Gaps = 44/624 (7%)

Query: 34 FDHINLEYSGLEKVNKAVAAGNXXXXXXXXXXXXXREKSKAREPDFSNAEKPADIRQPIDK 93
F+ INL Y GLEKV + AG R ++ P+ S I I +
Sbjct: 50 FEAINLNYPGLEKVKEFYEAGEHYAANALLEYYRTRTNVTNPNLSL-----INVTISE 103

Query: 94 VTREMADKALV-HQFQPHKGY-----GYFDYGKD--INWQMWPVKD--NEVRWQLHRVK 142
+ AD ALV ++F + Y + +D INW+ P KD +E + QLHR +
Sbjct: 104 AEQAKADYALVDYRFHVNNFYEDKETLKPYSVKQDGGINWEYSP-KDASDEYQKQLHRHQ 162

Query: 143 WWQAMALVYHATGDEKYAREWVYQYSDWARKNPLGLSQDNDKFVWRPLEVSDRVQSLPPT 202
W+ A Y +GDEKY + W+ Y +W NP + N W+ L+VS R+
Sbjct: 163 WFIPQAKAYRVSGDEKYIQSWIEVYKNWIENPNKPTTGPNTTSWWQ-LQVSTRIGDQVQL 221